AL49928 Streptoco
AX571762 Sequence
AX454068 Streptoco
AX454068 Streptoco
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AX954169 Sequence
CQ645750 Sequence
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CO6546 Streptoco
AE010027 Streptoco
Continuation (8 of
AX454070 Streptoco
AX454072 Streptoco
AX454072 Streptoco
AX454073 Streptoco
AX454073 Streptoco
AX454074 Streptoco
AX454077 Streptoco

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TITITGEGAATCGAATTCGAGCTCGCCCTCCTGACCACCTATNTGCATCAAGTGCCAAA 120
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Patent: WO 02061070-A 39 08-AUG-2002;
ID-Lelystad, Instituut voor Dierhouderij en Diergezondheid B.V.
(NL)
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Best Local Similarity 99.6%; Pred. No. 7.3e-71;
Matches 262; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
1. .263
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db xref="taxon:32630"
/nole="nucleotide sequence of ivs 31"
                                                                                                                                                                                                                                                                                        DNA
                                                                                                                                                                                                                                                                                                                                                 other sequences; artificial sequences
                                                                                                                                                                                                                                                                                       AX528970 263 bp
Sequence 39 from Patent WO02061070.
AX528970
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AE008461
SPREU1906
AX571762
AX57162
AX54665
AX554169
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AX5645750
AX50003-07
AE01003-07
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CP000017-07
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AY56303 Streptoco
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AR120267 Sequence
BD063276 Streptoco
AR340958 Sequence
AK568296 Sequence
AK568296 Sequence
AK58897 Sequence
AK58897 Sequence
AK11615 Sequence
AK21800 Sequence
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                                                                     (without alignments)
6924.422 Million cell updates/sec
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AF303227
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Gapop 10.0 , Gapext 1.0
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                                             nucleic search, using
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TITLE JOURNAL

FEATURES

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Arfalls Streptococcus suis fibronectin/fibrinogen binding protein (fbps) gene, complete cds; and alpha-acetolactate decarboxylase gene, partial cds.
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SVSNXDBIGDHIQATLJVBLMGKHSNIILVDKSBQKIIBAIKHGFSQNSYRTILPGS
SYSNXDBIGDHIQATLJVBEJMGKHSNIILVDKSBQKIIBAIKHGFSQNSYRTILPGS
STRIPPETRAPYTVQSDBKLFRILSTQELSPKNLQQVFGGLGRDTASELANHLQIDR
LKNFRAFFDQAICHTMSSYAALPFANSPBNQPHFBSSLSGLLDFYYQDKAEDRVAQ
QANELIKRVASELEKNRKKIIKQEQGLADTETAELVRQKGELLTTYLHQVPNDQSSVR
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THTGQASLABIDEIREELIETGYLKRHREKTHRQKPERIXIATDGKTIILVOKNNL
QNDELTFKMAKKGEIMFHAKDIPGSHVVITDNLDPSDEVKTDABLAAYFSKARHSNL
VQVDMIEAKKLHKPTGGKPGFVTYRGQKTLRVTPTEDKIKSMKIA
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de Greeff,A., Buys,H., Verhaar,R., Dijkstra,J., van Alphen,L. and
                      of FbpS Gene of Streptococcus suis
                                                                                                                                                        e of Veterinary Medicine, Nanjing
Tongwei Road, Nanjing, Jiangsu
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                                                                                                                                                                                                             Location/Qualifiers
1. 1938
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|mol type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="fbps"
/note="fn/fgn-binding protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
Sun, L., Fan, H. and Lu, C.
Cloning and Sequence Analysis of F.
Serctype 2 HA8801 Strain
Unpublished
2 (bases 1 to 1938)
Sun, L., Fan, H. and Lu, C.
Direct Submission
Sumitted (03-MAR-2004) College of Sqricultural University, No. 1 Ton 210095, P.R. China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="AAS67693.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            db xref="GI:45549556"
                                                                                                                                                                                                                                                                                                                                 /serotype="2"
/specific_host="swine"
/db_xref="taxon:1307"
/country="China"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Environmentally regulated genes of Streptococcus suis: identification by the use of iron-restricted conditions in vitro
TACTATACGGGCAAGGAACTGGAGATTGAGTTGGATGGGATGTGACTTCGACTCCTAGCCAAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTCCTGACCACCTATNTGCATCAAGTGCCAAATGACCAGTCGAGTGTGCGGTTAGACAAC
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Streptococcus suis
Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
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Smith, H.E., Buijs, H., de Vries R, R., Wisselink, H.J.,
Stockhofe-Zurwieden, N. and Smits, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 175;
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/clone="ivs 31"
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                                                                    CAAGGAGGCGGTCAAGCACCTGA 263
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DEFINITION

RESULT 3 AY566303

ORGANISM ACCESSION VERSION KEYWORDS SOURCE

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1200001 1310000
1300001 1410000
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CP000023 08/c
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L. Submitted (22-OCT-2001) Infectious Diseases and Food Chain Quality, ID-Lelystad, Edelhertweg 15, Lelystad NL-8219PH, The Netherlands in Location/Qualifiers

I. .2179

/ Organism="Streptococcus suis"
/ Mol_type="genomic DNA"
/ Abb_tref="genomic DNA"
/ Abb_tref="taxon:1307"
/ Abb_tref="ta
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SVSNKDBIGDHIQATLIVEINGKHSNIILDNDREDGKIIEATRHGEGSTREPES
SVSNKDBIGDHIQATLIVEINGKHSNIILDNDREDGKIIEATRHGEGSTRUFSEBANHLQUB
LIKNFRAFFDGATOGSTREKTERILETGETGEBENGUPHFEBLSELLDFYYQDKABRDRVAD
QANELIKRYASELEKORKKCLIKQEGELADTETAELVRQKGELLTTYVHQVPNDQSSYR
DTWLCQASLAEIBENDVALTFSGQNAGYFRKYQLKABAVHTIALIEETSKSIIVLTESY
DTWLCQASLAEIBENDVALTFSGQNAGYFRKYQLKABAVHTIALIEETSKSIIVLTESY
ONDELLFRMAKKGELWFHAKDIPGSSHVVITDNLDFSDEVKTDAAELAAYFSKARHSNI
VQVDMIERKCHKPTGGREGYTTRGQKTLRVTFTEBKIKKSNKI"
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VEVGPVDQLDQRFPVQDRQYLYAKFNAKEVREDIDKAE"
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                  Smith, H.R. Contribution of fibronectin-binding protein to pathogenesis of
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'product="fibronectin/fibrinogen binding protein"
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protein id="AAL85277.1"
db_xref="GI:19110787"
                                                                         Streptococcus suis serotype 2
Infect. Immun. 70 (3), 1319-1325 (2002)
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db_xref="GI:19110786"
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'rpt_type=inverted
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/gene="fbps"
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/gene="fbps"
235. .241
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/gene="fbps"
/note="FBPS"
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/gene="fbps"
136. .141
/gene="fbps"
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gene="fbps"
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Unclassified.
1 (bases 1 to 1423)
1 (bases 1 to 1423)
2 (Choi, G.H., Kunsch, C.A., Barash, S.C., Dillon, P.J., Dougherty, B., Fannon, M.R. and Rosen, C.A.
Streptococcus pneumoniae antigens and vaccines
Patent: US 6573082-A 59 03-UNN-2003;
Pluman Genome Sciences, Inc.; Rockville, MD
Location/Qualifiers
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C12N15/31, C12N5/18, C12N1/21, C07K14/315, C12Q1/68, A61K39/09,
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Best Local Similarity 67.8%; Pred. No. 1.9e-15;
Matches 118; Conservative 0; Mismatches 56; Indels
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                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 59 from patent US 6573082.
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Sequence 59 from patent US 6887663.
                                                                                                                                               /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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/organism="unknown"
/mol_type="genomic DNA"
                                                                                                                Location/Qualifiers
                                                       Strandedness: Double;
Topology: Linear;
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                 G01N33/569,
PC G01N33/68
CC Strandednes
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Kunsch, C.A., Choi, G.H., Johnson, S.L. and Hromockyj, A.
Streptococcus pneumoniae antigens and vaccines
Patent: JP 2001505415-A 30 24-APR-2001;
HUMAN GENOME SCIENCES INC
PN JP 2001505415-A/30
PN 24-APR-2001
PR 30-OCT-1997 UP 1998520667
PR 31-OCT-1997 US 60/029960
PR ALCT-1996 US 60/029960
PR GHARLES A KUNSCH, GIL H CHOI, SYDNOR L JOHNSON, ALEX HROMOCKYJ PC
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                                     89 CTCCTGACCACCTAINTGCATCCAAGTGCCAAATGACCAGTCGAGTGTGCGGTTAGACAAC
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Streptococcus pneumoniae antigens and vaccines.
BD063276
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Choi,G.H., Kunsch,C.A., Barash,S.C., Dillon,P.J
Fannon,M.R. and Rosen,C.A.
Streptococcus pneumoniae antigens and vaccines
Patent: US 6159469-A 59 12-DEC-2000;
Location/Qualifiers
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/mol_type="unassigned DNA"
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JP 2001505415-A/30.
unidentified
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                                                                                                                                                                                                                                                                                                                                    Sequence 59 from patent
ARI20267
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Best Local Similarity 67.8
Matches 118; Conservative
 Matches 124; Conservative
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/organism="unknown"
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Matches 118; Conservative
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                                                                                                                                                                   Barash, S.C., Dillion, P.J., Dougherty, B.,
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 85; DB 6; Length 1423;
Pred. No. 1.9e-15;
0; Mismatches 56; Indels
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Pred. No. 1.9e-15;
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Choi.G.H., Kunsch.C.A., Barash,S.C., Dillion,P. Choi.G.H., Kunsch.C.A., Barash,S.C., Dillion,P. Streptococcus pneumoniae SP036 polynucleotides Patent: US 6897663-A. 59 03-MAY-2005, Human Genome Sciences, Inc.; Rockville, MD Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:1313"
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/mol_type="genomic DNA"
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Unclassified.
Unclassified.
(base to 1692)
Doucette-Stamm, L.A. and Bush, D.
Nucleic acid and amino acid sequences relating to Streptococcus penemoniae for diagnostice and therapeutics
Patent: US 6800744-A 1976 05-0CT-2004;
Genome Therapeutics Corporation; Waltham, MA
                                                                                                                                                                                                                                                     Houseweart, C.B.
Nucleic acid and amino acid sequences relating to Streptococcus
pneumoniae for diagnostics and therapeutics
Patent: US 6699703-A 2519 02-MAR-2004;
Genome Therapeutics Corporation; Waltham, MA
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Doucette-Stamm, L., Bush, D., Zeng, Q., Opperman, T. and
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Pred. No. 1.9e-15;
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67.8%; Pred. No. 1.9e-15
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Sequence 1976 from patent US 6800744.
ARS87857
  AR481615 1683 bp DN.
Sequence 2519 from patent US 6699703.
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/mol_type="genomic DNA"
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gene, complete cds.
AP181976.
AP181976.1 GI:6175914
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1 (bases 1 to 2015)

Holmes,A.R., McNab,R., Millsap,K. and Jenkinson,H.F.

The pavA gene of Streptococcus pneumoniae encodes a adhesion and virulence tibronectin-binding protein that is necessary for Pneumococcal cell upublished

2 (bases 1 to 2015)

Holmes,A.R., McNab,R. and Jenkinson,H.F.

Direct Submission

Submitted (31-AUG-1999) Oral Sciences and Orthodontics, University of Otago, Great King St, Dunedin, New Zealand

Location/Qualifiers
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TYIAPPSTESINPFTIKOBKIPBILQTQBLTAKNLQSLFQGLGRDTANELERILVSEK
SELIRVAVENBLQKNRHGLKKQBRELLATDNABEPRANISDLIDTYKKNKARBRDKVKQA
SELIRVAVENBLQKNRHGLKKQBRELLATDNABERGKGELLTTFLHQVPNDQDQVILD
NYYTNQPIMIALDKNALTPNQNAQRYFKRYQKLKEAVKYLTDLIEBTKATILYLESVET
VLNQAGLEBTARIREBLIQTGFRRKQRKLQKKKLGQYLABDGKTIIYUGN
BELIFKWARKEBLMFRAKDIPGSRKVISONLDPSDAVKTDAABLAAYFSQGRLSNLVQ
VDMIEWKALNKFTGGKRGFVTYTGQKTLRVTDDSKKASMKGS
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SHRLLLSAHPVFGRIQLTQTTFENPAQPSTFIMVLRKYLQGALIESIEQVENDRIVEI
TVSNKNEIGDHIQATLIIEIMGKHSNILLVDKSSHKILEVIKHVGFSQNSYRTLLPGS
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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protein_id="AAF06332.1"
db_xref="G1:6175915"
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/organism="Streptococcus pneumoniae"
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/strain="RR900"
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/function="adhesin"
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210 CCCAGCGGTACTTCAAGAAGTACCAGAACTCAAGGAGGCGGTCAAGCACCTGA
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2e-15;
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    .10240
    /organism="unidentified"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32644"

                                                                                                                         CQ788941
Sequence 32 from Patent EP1400592.
CQ788941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                                                                                                                                                                                                           unclassified sequences.
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32.3%;
Best Local Similarity 67.8%;
Matches 118; Conservative C
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(without alignments)
3713.589 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Abs59824 Streptoco	Aav27353 Streptoco	Abq84821 S. pneumo	Adc45140 S. pneumo	Adm91909 S pneumon	Abx06664 S. pneumo	Aas55569 Streptoco	Aca49876 Prokaryot	Adk46004 Streptoco	Adr93341 Novel S.	Aea57211 Streptoco	Aav52165 Streptoco	Continuation (8 of	Continuation (9 of	Aca50476 Prokaryot	Abn67397 Streptoco	Aca48071 Prokaryot	Abn67396 Streptoco	Adv84865 Streptoco
	di 8	6 ABS59824	2 AAV27353	6 ABQ84821	10 ADC45140	12 ADM91909	10 ABX06664	4 AASSSS69	8 ACA49876	13 ADK46004	13 ADR93341 .	14 AEA57211	2 AAV52165	10 ABS56454 07	10 ABS56454 08	8 ACA50476 _	6 ABN67397	8 ACA48071	6 ABN67396	13 ADV84865
	Query Match Length DB	263	1423	1423	1423	1653	1680	1683	1683	1683	1692	1692	10240	110000	110000	1653	1728	1647	1653	1656
*	Query	99.0	32.3	32.3	32.3	32.3	32.3	32.3	32.3	32.3	32.3	32.3	32.3	32.3	32.3	31.6	31.6	29.0	25.4	25.4
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33	55.4	21.1	3792	~	AAQ48463	
	55.4	21.1	4784	œ	AAD51075	pOThy12
	55.4	21.1	4936	œ	AAD51076	pOThy15
	55.4	21.1	4995	æ	AAD51077	pOThy16
	55.4	21.1	4998	œ	AAD51074	
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c 45	20	19.0	6722	N	AAQ48465	Aaq48465 Plasmid p
					ALIGNMENTS	
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ID ABS	59824 B	tandar	ABS59824 standard; DNA;	263	BP.	

Modulating the virulence of a Streptococcus for the diagnosis of and vaccination against streptococcal infections, comprises the modification of a genomic fragment of Streptococcus suis. Streptococcus virulence; iron-restricted induced gene; iri; vaccine; in vivo selected gene; ivs; gene; ds. Streptococcus suis in vivo selected sequence (IVS), gene #30. (IDLE-) ID-LELYSTAD INST DIERHOUDERIJ EN DIERGEZ. Disclosure; Fig 6D1; 108pp; English. 31-JAN-2002; 2002WO-NL000073. 02-FEB-2001; 2001EP-00200419. (first entry) WPI; 2002-619248/66. Streptococcus suis. WO200261070-A2. 08-AUG-2002 Smith HB;

The invention relates to a method of modulating Streptococcus virulence by modifying a genomic fragment of it, where the genomic fragment comprises at least a functional part identifiable by hybridisation in Streptococcus suis to a nucleic acid or fragment of iron-restricted induced (iri) or in vivo selected (ivs) genes given in the specification, and obtaining a clone where the genomic fragment has been modified. The method is useful in modulating the virulence of Streptococcus suis that

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may be used in the diagnosis of and vaccination against streptococcal infections and in the detection of virulence markers of Streptococci. The vaccine comprising the clone, nucleic acid, vector, or the host cell, is also useful in the prevention and/or treatment of streptococcal infections. ABSS5982 represent Streptococcus suis in vivo selected (1vs) genes and related PCR primers of the invention
                                                                                                                                                                                                                                                       TTTTTGTGAATCGAATTCGAGCTCGCCCCTCCTGACCACCTATNTGCATCAAGTGCCAAA 120
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                                                                                                                                    DB 6; Length 263;
                                                                                                                                   Score 260.4; DB 6; Length
Pred. No. 9e-79;
0; Mismatches 1; Indels
                                                                                                                                                                                            1 ACGAAAATDGATGGATCCATGCATAAACTGCATCCCTTAACTTGTT
                                                                                                       Sequence 263 BP; 72 A; 63 C; 61 G; 66 T; 0 U; 1 Other;
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/*tag= a
/product= "SP0039"
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Best Local Similarity 99.6%;
Matches 262; Conservative (
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P-PSDB; AAW55092.
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The present sequence encodes a protein from Streptococcus pneumoniae. The nucleic acid sequence encoding the Streptococcus pneumoniae protein can be useful in vaccines for inducing protective antibodies against Streptococcus pneumoniae, for treatment or prevention of infection e.g. pneumonia, otitis media or meningitis. Probes based on the nucleic acid are used to detect Streptococcus infection (by usual hybridisation or amplification methods), also for isolating Streptococcus genes or their albit variants. The protein can be used similarly to detect specific antibodies in standard immunoassays, especially for diagnosing or monitoring infections. Antibodies which bind the protein are used to detect corresponding antigens, to purify the protein and for passive immunisation (optionally coupled to a toxin). Vaccines are administered, e.g. by injection, orally or through the skin, typically at 0.01-1000
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antibacterial; Streptococcal infection; detection; gene; ds
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                                                                                                                                                                                                                                                                                                      Length 1423;
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                                                                                                                                                                                                                                                                                                     32.3%; Score 85; DB 2; 167.8%; Pred. No. 3.3e-18; ative 0; Mismatches 56.
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              Claim 1; Page 60-61; 118pp; English
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Matches 118; Conservative
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KUNSCH C A.
BARASH S C.
DILLON P J.
DOUGHERTY B.
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P-PSDB; ABP54586.
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Query Match 32.3
Best Local Similarity 67.8
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30-0CT-1997;
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Rosen CA;
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The invention relates to an isolated polynucleotide consisting of a Streptococcus pneumoniae nucleic acid (appearing as ADC45122 and encoding SP028) one of 113 disclosed nucleic acids encoding 113 S. pneumoniae antigens. Also included are making a recombinant vector by inserting the nucleic acid into a vector, an isolated polynucleotide consisting of at least 50 or 100 contiguous nucleotides of the SP028 nucleic acid, and a recombinant host cell comprising the SP028 polynucleotide. The nucleic acids are useful as DNA vaccine against Streptococcus pneumoniae infection (e.g. pneumonia). Nucleic acids derived from the S. pneumoniae antigen nucleic acids are useful as probes for use in diagnostic methods for detecting S. pneumoniae gene expression. The present sequence encodes an S. pneumoniae antigenic protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   150 ACTATACGGGCAAGGAACTGGAGATTGAGTTGGATGTGGCTTTGACTCCTAGCCAAAATG 209
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                                                                                                                                                                                                                                                                                                                                                                                                              90 TCCTGACCACCTATNTGCATCAAGTGCCAAATGACCAGTCGAGTGTGCGGTTAGACAACT
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                                                                                                                                                                                                                                                                                                                             Length 1423;
                                                                                                                                                                                                                                                                                 Sequence 1423 BP; 488 A; 324 C; 281 G; 330 T; 0 U; 0 Other;
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Pred. No. 3.3e-18;
                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADM91909 standard; DNA; 1653
                                                                                                                                                                                                                                                                                                                             Query Match 32.3%;
Best Local Similarity 67.8%;
Matches 118; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TUFT ) UNIV TUFTS.
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                                                                                                                                                            ABQ84792 to ABQ84904 represents nucleic acids which encode the Streptococcus pneumoniae antigens given in ABP84557 to ABP54669. The S. pneumoniae antigens have antibacterial activity and can be used in vaccines. The S. pneumoniae antigens can also be used to prevent or attenuate a Streptococcal infection in an animal. The polymucleotides encoding the S. pneumoniae antigens can be used to detect Streptococcus nucleic acids. ABQ84905 to ABQ8130 represent primers used in the cloning of S. pneumoniae QRFs (open reading frames) which are used in an example
                 New Streptococcus pneumoniae antigens, useful for detecting Streptococcus and for preventing or attenuating disease caused by Streptococcus infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCCTGACCACCTAINTGCATCAAGTGCCAAATGACCAGTCGAGTGTGCGGTTAGACAACT 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      776
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       777 actataccaccaacctatcatgattgcgcttgataaggctctgactccaaccagaatg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         717 recreaceacerrecreceaceasiseceraaceaceagerrarecrasser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCCAGCGGTACTTCAAGAAGTACCAGAACTCAAGGAGGCGGTCAAGCACCTGA 263
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                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1423 BP; 488 A; 324 C; 281 G; 330 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                           DB 6; Length 1423;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           Score 85; DB 6; I
Pred. No. 3.3e-18;
0; Mismatches 56;
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    S. pneumoniae DNA encoding antigen SP039.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              멾
                                                                                                                           Claim 1; Page 28; 70pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-MAR-2000; 2000US-00536784.
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97US-00961083
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                                                                                                                                                                                                                                                                                                                                                                                                                           32.3%;
                                                                                                                                                                                                                                                                                                                                        from the present invention
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This invention relates to novel isolated Streptococcus pneumoniae nucleic acid molecules and the antigenic polypeptides encoded by them. The invention may be useful for the production of compounds with an antibacterial activity or for gene therapy. The nucleic acid molecules, compositions and methods disclosed are useful for treating Streptococcus

Disclosure; SEQ ID NO 106; 123pp; English.

encoding Streptococcus pneumoniae polypeptides vaccines for prevention or attenuation of infection

polynucleotide encoding

Novel

P-PSDB; ADC45141.

by Streptococcus pneumoniae.

for producing

Example 1; SEQ ID NO 59; 58pp; English.

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                                                                                                                                                                                                                                                                 1006
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                                                                                                                                                                                                                                                                                                                   209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New proteins and nucleic acid molecules from Streptococcus pneumoniae, useful as medicaments for treating or preventing a disease or infection due to streptococcus bacteria, such as pneumonia, sepsis, otitis media or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a protein comprising or having at least 50% identify to any of the 2469 amino acid sequences, identified in the specification (available on a computer readable format), or its fragment, expressed from 2469 of 2489 identified DNA coding regions from the Streptococcus pneumoniae type 4 strain genomic sequence appearing as ABS56454. Also included are an antibody which binds one of the proteins, treating a patient by administering the protein, DNA or antibody (in a composition), a kit comprising first and second primers, which are the neuclast card cited above or fragments between nucleotides 8-100 of a sequence not defined in the specification, for amplifying a target sequence contained within a Streptococcus nucleic acid sequence, where
                                                                                                                                                                                                                   90 TCCTGACCACCTAINTGCATCAAGTGCCAAATGACCAGTCGAGTGTGCGGTTAGACAACT
                                                                                                                                                                                                                                                              947 recreacaracerrecrecaceargecerareaceaceargerrarecragacarer
                                                                                                                                                                                                                                                                                                                   150 ACTATACGGGCAAGGAACTGGAGATTGAGTTGGATGTGGCTTTGACTCCTAGCCAAAATG
pneumoniae infection. The present sequence is that of an S pneumoniae
                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                  263
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                                                                                                                                                                                                                                                                                                                                                                                                                  CCCAGCGGTACTTCAAGAAGTACCAGAAACTCAAGGAGGCGGTCAAGCACCTGA
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                                                                                                                       Length 1653;
                                                                    Seguence 1653 BP; 551 A; 383 C; 322 G; 397 T; 0 U; 0 Other;
                                                                                                                                                                     56; Indels
                                                                                                                  Score 85; DB 12;
Pred. No. 3.6e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pneumoniae type 4 strain coding region #952
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                                                                                                   32.3%; Bcc. No. 5...
67.8%; Pred. No. 5...
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABX06664 standard; DNA; 1680 BP
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                                                                                                                                                                  Matches 118; Conservative
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                      gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (revised)
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                                                                                                               Query Match
Best Local Similarity
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11-FEB-2003
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the first primer is substantially complementary to the target sequence and the second primer is substantially complementary to the complement of the target sequence, and where the parts of the primers having substantial complementarity define the termin of the target sequence to substantial complementarity define the termin of the target sequence to be amplified, assay comprising contacting a test compound with the protein, and determining whether the test compound binds to the protein and a Streptococcus pneumoniae bacterium, where one or more genes encoding the proteins has been rendered inactive. The proteins, nucleic caid molecules, antibody and compositions are useful as medicaments for treating or preventing a disease or infection due to streptococcus bacteria, particularly S. pneumoniae, such as pneumonia, sepsis, otitis bacteria and antibiocics. The methods are useful for identifying immunodominant proteins. The present sequence is one of the 2489 confinential for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   974 recreacaaccircciccaccaagreccraaccaaccaagaccaggirarccragacaacr 1033
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90 TCCTGACCACCTATNTGCATCAAGTGCCAAATGACCAGTCGAGTGTGCGGTTAGACAACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus pneumoniae DNA for cellular proliferation protein #140.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCCAACGCTATTTTAAACGGTATCAGAAACTCAAAGAAGCTGTCAAATACTTGA 1147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antisense; ds; prokaryotic cellular proliferation gene; antibiotic; antibacterial; drug design.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1680;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1680 BP; 564 A; 387 C; 329 G; 400 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 10;
3.6e-18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 3.6e-
0; Mismatches
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2000US-024257BP.
2000US-0253625P.
2000US-0253625P.
2000US-025393P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32.3%;
67.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 67.8
Matches 118; Conservative
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26-MAY-2000;
23-OCT-2000;
27-NOV-2000;
22-DEC-2000;
16-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-MAR-2000;
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Yamamoto RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-SEP-2001
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(ELIT-) ELITRA PHARM INC.
                                                                Zamudio C,
Trawick JD,
                                                                                                                                                                    WPI; 2003-029926/02
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                                                                   Wang L,
Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 9
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                                                                                                                                                                                                                                                              The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, the prokaryotic cellular proliferation, their use in identifying the genes, the their use in the discovery of novel antibiotics, the essential genes coll, Staphylococcus aureus, Salmonella typhi, Klebsialla pneumoniae, rosful, Staphylococcus aureus, Salmonella typhi, Klebsialla pneumoniae, coll, Staphylococcus and Enterococcus faecalis. The invention is also be useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antisense nucleic acids caids the expressed proteins. The proteins con the proteins can also be used to screen compounds in rational drug discovery programmes. The cantisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein. Mote: The sequence data for this patent control form part of the printed specification, but was obtained in the form part of the printed specification, but was obtained in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1034 ACTATACCAACCAACCTATCATGATTGCGCTTGATAAGGCTCTGACTCCCAACCAGAATG 1093
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     150 ACTATACGGGCAAGGAACTGGAGATTGAGTTGGATGTGGCTTTGACTCCTAGCCAAAATG 209
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                                                                                                       New polynucleotides for the identification and development of antibiotics, comprise sequences of antisense nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1683 BP; 565 A; 387 C; 331 G; 400 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4; Length 1683;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56; Indels
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Pred. No. 3.6e-18;
0; Mismatches 56
                                                                                                                                                                                                               Claim 27; SEQ ID NO 9206; 511pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Prokaryotic essential gene #31533.
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2001US-0342923P.
2002US-00072851.
2002US-0362699P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 32.3%;
Best Local Similarity 67.8%;
Matches 118; Conservative
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          2001-611495/70.
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          WPI; 2001-611495/
P-PSDB; AAU37710
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25-OCT-2001;
08-PEB-2002;
06-MAR-2002;
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the invention trainers to an inviter active where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

Co the nucleic acid inhibits proliferation of a cell. Also included are:

Co the nucleic acid inhibits proliferation of a cell. Also included are:

Co (1) a vector comprising a promoter operably linked to the nucleic acid
encoding a polypeptide whose expression is inhibited by the antisense

Co nucleic acid; (2) a host cell containing the vector; (3) an isolated

Co contisense nucleic acid; (4) an antibody capable of specifically binding

Co polypeptide, (5) producing the polypeptide; (6) inhibiting cellular

Co proliferation or the activity of a gene in an operon required for

Co proliferation or that has an activity against a biological pathway

Co the gene product or that has an activity against a biological pathway

Co required for proliferation, or that inhibits cellular proliferation; (8)

Co identifying a gene required for cellular proliferation of an

Co pathway in which a proliferation-required gene or its gene product lies

Co a gene on which the test compound that inhibits proliferation of an

Corganism acts; (9) manufacturing an antibiotic; (10) profilling a

Compound's activity; (11) a culture comprising strains in which the gene

Crompound's activity; (11) a culture comprising strains in which the gene

Crompound's activity; (11) a culture comprising strains in which the gene

Crompound's activity; (11) a culture comprising strains in which the gene

Crompound's activity; (12) dentificant of a compound that inhibits the

Crompound's activity; (13) identifying the target of a compound that inhibits the

Crompound's activity; (11) a culture comprising strains in which each of the strains is present in a culture or collection of

Crompound and organism. The antisense nucleic acids are useful for

Crompound and organism. The areal activity of acids ac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention relates to an isolated nucleic acid comprising any one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90 TCCTGACCACCTAINTGCATCAAGTGCCAAATGACCAGTCGAGTGTGCGGTTAGACAACT
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Zyskind JW;
Xu HH;
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                                                                                                                                                                                                                                                                New antisense nucleic acids, useful for identifying proteins or s
for homologous nucleic acids required for cellular proliferation
isolate candidate molecules for rational drug discovery programs.
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    Ohlsen KL,
Forsyth RA,
    Haselbeck R,
Yamamoto R,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 14; SEQ ID NO 37746; 1766pp; English
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         Malone C,
Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADK46004 standard; DNA; 1683
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Best Local Similarity 67.8°
Matches 118; Conservative
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The invention relates to an isolated nucleic acid comprising a sequence encoding a Streptococcus pneumoniae ADR91366polypeptide, or its fragments, with any of 5 fully defined sequences depearing as ADR94308, ADR94489, ADR94807, ADR94806, ADR948255, ADR95262, ADR95682, ADR948079, ADR94807, ADR94809, ADR94809, ADR94807, ADR94809, ADR94806, ADR95263, ADR95682, ADR95197, ADR92197, ADR92186, ADR92197, ADR92197, ADR92197, ADR92186, ADR92197, ADR92197, ADR92186, ADR92187, ADR92197, ADR92187, ADR921870 and ADR9218880 ADR92188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated nucleic acid encoding a Streptococcus pneumoniae polypeptide, useful for diagnosing, preventing and/or treating pathological conditions resulting from the bacterial infection.
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Pred. No. 3.6e-18;
0; Mismatches 56; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 1976; 151pp; English.
                                                                                                                                                                                                                                                                                       (GENO-) GENOME THERAPEUTICS CORP.
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98US-0085131P.
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Matches 118; Conservative
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                           JS6800744-B1
                                                                                                                                             30-JUN-1998;
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12-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to isolated Streptococcus pneumoniae nucleic acids and polypoptides. The nucleic acids and proteins are useful for diagnosing, preventing and treating pathological conditions resulting from bacterial infection, such as S. pneumoniae infection. These may also be used for drug screening procedures. The present sequence represents a Streptococcus pneumoniae nucleic acid of the invention. Note: The sequence data for this parent did not appear in the printed specification but was obtained in electronic format directly from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         149
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                                                         ds; gene; Antibacterial; Gene therapy; Vaccine; Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid molecules and polypeptides useful for diagnosing, preventing and treating pathological conditions resulting from bacterial infection, e.g. Streptococcus pneumoniae infection, and in drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90 TCCTGACCACCTATNTGCATCAAGTGCCAAATGACCAGTCGAGTGTGCGGTTAGACAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  974 TGCTGACAACCTTCCTCCACCAAGTGCCTAACGACCAAGACCAGGTTATCCTAGACAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           150 ACTATACGGGCAAGGAACTGGAGATTGAGTTGGATGTGGCTTTGACTCCTAGCCAAAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1034 ACTATACCAACCAACCTATCATGATTGCGCTTGATAAGGCTCTGACTCCCAACCAGAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Opperman T, Houseweart CE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCCAGCGGTACTTCAAGAAGTACCAGAAACTCAAGGAGGCGGTCAAGCACCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1683 BP; 563 A; 386 C; 332 G; 402 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 32.3%; Score 85; DB 13; Length 16 Local Similarity 67.8%; Pred. No. 3.6e-18; les 118; Conservative 0; Mismatches 56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Meningitis; bacteraemia; pneumonia; otitis media; ds;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel S. pneumoniae DNA sequence, SEQ ID 1976.
Streptococcus pneumoniae gene, Seq ID No 2519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 2519; 301pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zeng Q,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GENO-) GENOME THERAPEUTICS CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       segdata.uspto.gov/seguence.html.
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                                                                                                                                                                                                                                                                                                                                                                                                            98US-00107433.
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                                                                                                                                                                                                                                                                                                                                                97US-0051553P.
98US-0085131P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                  Streptococcus pneumoniae
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                                                                                                                                                                        US6699703-B1
                                                                                                                                                                                                                                                                                                                                                                           12-MAY-1998;
30-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                02-JUL-1997;
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Query Match Matches

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RESULT 10 ADR93341

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1042

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Gaps

1043 ACTATACCAACCAACCTATCATGATTGCGCTTGATAAGGCTCTGACTCCCAACCAGAATG 1102

셤 ò 셤

1103 CCCAACGCTATTTTAAACGGTATCAGAAACTCAAAGAAGCTGTCAAATACTTGA 1156

210 CCCAGCGGTACTTCAAGAAGTACCAGAAACTCAAGGAGGCGGTCAAGCACCTGA

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The invention relates to an isolated nucleic acid molecule for detecting, preventing or treating pathological conditions resulting from bacterial preventing or treating pathological conditions resulting from bacterial infection. The isolated nucleic acid comprises: (a) any of the 2603 mucleotide sequences of ARA57836 to ARA57838; (b) a nucleotide sequence encoding a Streptococcus pneumoniae polypeptide comprising any of the cacid sequences of ARA57839; (b) a nucleotide sequence of at least 8 nucleotides in length, where the sequence is hybridizable to a nucleic taid having any of the nucleotide sequence is chybridizable to a nucleic taid having any of the nucleotide sequence is chybridizable to a nucleic taid having any of the nucleotide sequence is chown nucleic acid operably linked to a transcription regulatory element; (c) a cell comprising the recombinant expression vector comprising the conditions of a probe comprising a nucleotide sequence consisting of at least 8 nucleotides of ARA57838; (5) treating a subject for S. pneumoniae infection, (6) a recombinant or substantially pure preparation of an S. pneumoniae polypeptide; (7) a vaccine composition for preventing or treating an S. pneumoniae (8) a computer readable medium having recorded the nucleotide sequences of ARA55236 to ARA57838; (10) a computer readable medium having recorded the nucleotide sequences of ARA55336 to ARA57838; (10) a computer readable medium having recorded the nucleotide sequences of ARA55336 to ARA57838; (10) a computer based system for identifying cramming of the Streptococcus genome of commercial infection. The present composition and methods are useful for diagnosing, preventing or treating bacterial infections, particularly S. pneumoniae infection. The present composition for he seminence and for his naterial did not form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               present invention. Note - The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO web site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid molecules and encoded polypeptides useful for diagnosing, preventing or treating bacterial infections, particularly Streptococcus pneumoniae infection.
                                                                                            bacterial infection; Streptococcus pneumoniae infection; antibacterial;
Streptococcus pneumoniae ORF nucleic acid sequence SEQ ID NO:1976.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 1976; 144pp; English
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98US-0085131P.
98US-00107433.
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                                                                                                                                                                                                                                                    Streptococcus pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bush
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Doucette-Stamm LA,
                                                                                                                                                       vaccine; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-JUL-1997;
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30-JUN-1998;
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The present invention describes a computer readable medium which has the nucleotide sequences SEQ ID NO:1 to 391 (AAV52134 to AAV52524) recorded on it, or a representative fragment or a sequence at least 95% identical to SEQ ID NO: 1 to 391. The nucleotide sequences depicted in SEQ ID NO:1 to 391 (AAV52134 to AAV52524) are genomic fragments from Streptococcus pneumoniae. The present invention also describes an isolated mucleic acid colecule encoding a homologue of any of the fragments of the S. pneumoniae or genome (SEQ ID NO:1 to 391) where the nucleic acid molecule is produced by a process comprising: (a) screening a genomic DNA library using as a process comprising: (a) screening a genomic DNA library using as a process comprising: (a) screening a genomic DNA library using as a process comprising: (b) isolating many of the sequences in SEQ ID NO:1 to 391, identifying members of the library which contain sequences that hybridise to the target sequence and isolating the nucleic acid molecules or corganism, amplifying nucleic acid molecules whose nucleic acid molecules or corganism, amplifying nucleic acid molecules whose nucleotide sequence is consumeriae genome to prime the amplification and isolating the amplified sequences. The computer readable medium can be used in a computer-based system for identifying fragments of the S. pneumoniae genome. Produces from the present invention can be used in commercial importance, or expression modulating fragments of the S. pneumoniae genome. Produces from the present invention can be used in computer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90 TCCTGACCACCTAINTGCATCAAGTGCCAAATGACCAGTCGAGTGTGCGGGTTAGACAACT 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Computer-readable medium with recorded Streptococcus pneumoniae polymucleotide sequences - useful in diagnostic kits and assays, and pharmaceutical compositions and vaccines for Streptococcus pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fannon M;
                                                                                                                                                                                                         S. pneumoniae; genome; diagnosis; assay; vaccine; pharmaceutical composition; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10240 BP; 2865 A; 1914 C; 2390 G; 3068 T; 0 U; 3 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Barash SC,
                                                                                                                                                                    Streptococcus pneumoniae genome fragment SEQ ID NO:32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 326-332; 1409pp; Bnglish.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dillon PJ,
                                       AAV52165 standard; DNA; 10240 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                Streptococcus pneumoniae; computer readable medium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 67.8 Matches 118; Conservative
                                                                                                                                                                                                                                                                                Streptococcus pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Choi GH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1998-272225/24.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dougherty BA;
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                                                                                                                              23-OCT-1998
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                                                                                      AAV52165;
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RESULT 12
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150 ACTATACGGGCAAGGAACTGGAGATTGAGTTGGGCTTTGACTCCTAGCCAAAATG

90 TCCTGACCACCTAINTGCATCAAGTGCCAAATGACCAGTCGAGTGTGCGGTTAGACAACT 149

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Gaps

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56; Indels

Pred. No. 3.6e-18; 0; Mismatches 56

32.3%; Score 85;

67.8%;

Best Local Similarity 67.8 Matches 118; Conservative

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Query Match

DB 14; Length 1692;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated nucleic acid comprising any one of
the 6213 antisense sequences given in the specification where expression
of the nucleic acid inhibits proliferation of a cell. Also included are:
                                                                                                                                                                                                                                                                   1423 ACTATACCAACCAACCTATCATGATTGCGCTTGATAAGGCTCTGACTCCCAACCAGAATG
                                                                                                                                                                                                                                                     150 ACTATACGGGCAAGGAACTGGAGATTGAGTTGGATGTGGCTTTGACTCCTAGCCAAAATG
                                                                                                                                                                                                    90 TCCTGACCACCTATNTGCATCAAGTGCCAAATGACCAGTCGAGTGTGCGGTTAGACAACT
                                                                                                                                                                                                                            7483 TGCTGACGACCTTCCTCCACCAAGTGCCTAACGACCAAGACCAGGTTATCCTAGACATT
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Xu HH;
                                                                                                                                                                                                                                                                                                                             7310
                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New antisense nucleic acids, useful for identifying proteins or scre
for homologous nucleic acids required for cellular proliferation to
isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                     CCCAGCGGTACTTCAAGAAGTACCAGAAACTCAAGGAGGCGGTCAAGCACCTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antisense, ds; prokaryotic essential gene, cell proliferation;
drug design; gene.
                                                                                                                                                 Length 110000;
                                                                                                                                                                           56; Indels
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Forsyth RA,
                                                                                                                                                  Score 85; DB 10;
Pred. No. 2.3e-17;
0; Mismatches 56
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Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 14; SEQ ID NO 38346; 1766pp; English.
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1710000
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2110000
              1310000
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Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; 2001US-00815242.
; 2001US-00948993.
; 2001US-0342923P.
; 2002US-00072851.
; 2002US-0362699P.
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                                                                                                                                                    32.3%;
67.8%;
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1600001
              1200001
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                                                                                                                                                    Query Match 32.3
Best Local Similarity 67.8
Matches 118; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus pyogenes
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Trawick JD,
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  ABS56454 11
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08-FEB-2002; 2
06-MAR-2002; 2
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06-SEP-2001;
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ACTATACGGGCAAGGAACTGGAGATTGAGTTGGATGTGGCTTTGACTCCTAGCCAAAATG
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WP Sequence aplit into 2:
WP PRS56454 00
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WP ABS56454 01
WP ABS56454 03
WP ABS56454 04
WP ABS56454 06
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cc (1) a vector comprising a promoter operably linked to the mucleic acid encoding a polypeptide whose expression is inhibited by the antisense conclains acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding callusar proliferation or the activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for proliferation, or that has an activity against a bloolgical pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product or the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound sactivity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent or organism; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for considence or in a gene on which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for cellular proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is one of the target contradistation, but was obtained in the printed generication, but was obtained in cells requences
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93 TGACCACCTAINTGCATCAAGTGCCAAATGACCAGTCGAGTGTGCGGTTAGACAACTACT 152

Best Local Similarity 68.09 Matches 115; Conservative

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Query Match

Gaps ; 0 1007 ATACAGGGGAAAAAATTGAGATTGCCTTAGACAAGGCTCTGACACCAAATCAAAATGCTT 1066

153 ATACGGGCAAGGAACTGGAGATTGAGTTGGATGTGGCTTTGACTCCTAGCCAAAATGCCC 212

Search completed: January 20, 2006, 15:20:15 Job time : 475 secs

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January 20, 2006, 14:03:25; Search time 3837 Seconds (without alignments) 3206.933 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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9b_est2::*
9b_htc::*
9b_est4::*
9b_est6::*
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	BY453899 BY453899 CB898978 trico16xm AL067834 Brosophil BX368104 BX368104 CV072680 Lr_JV2CF CX036082 Lr_JV2CF CX036082 Lr_JV3CF BM63883 170006873 BM63683 170006874 BM62684 170006874 BM628044 170006874 BM628044 170006874 BM62804 170006874 BM62804 170006874 BM62804 170006874 BM62804 170006873 BM642729 170006873 BM649206 170006873 BM649206 170006873 BM649206 170006873 BM649206 170006873 BM649206 170006873 BM64804 170006873 BM64804 170006873 BM64804 170006873
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3 BM651776 3 BM625442 3 BM643948 3 BM653819	3 BM656762 3 BM631562 3 BM592722 3 BM641312 3 BM646862	3 BM627009 10 CG618897 5 BX848199 3 BJ686992 9 AZ108235	6 CA449674 2 BE970931 1 AW553179 2 BG146742	4664
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ALIGNMENTS	BY453989 BY453989 RIKEN full-length enriched, pooled tissues, adult spleen, etc. Mus musculus cDNA clone K630070L23 3', mRNA sequence. BY453989. BY453989. BY453989. BY453989. GI:26750723 BST. Mus musculus (house mouse) Mus musculus (house mouse) Mus musculus (house mouse) Mus musculus (house mouse) Scharyota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Burarchoncoglires; Glires; Rodentia; Sciurognathi; Muroides; Murinae; Mus.	l (bases 1 to 428) Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Kiyosawa, H., Yaqi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Batalov, S., Balase, J.M., Kanapin, A., Matsuda, H., Batalov, S., Belsel, K. W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.B., Cousins, S., Dallas, B., Dragani, T.A., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarris, B.D., Kanal, A., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kaurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Nantais, L., Marchionni, L., McKenzie, L., Miki, H., Naqashima, T., Nantais, L., Marchionni, L., McKenzie, L., Miki, H., Naqashima, T., Nawasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Schneider, C., Semple, C., R., Setcou, M., Shimada, K., Sandelin, A., Schneider, C., Sample, C., Rangchand, R., Yang, L., Yuan, Z., Zavolam, M., Zhangtawa, M., Yang, L., Yuan, Z., Zavolam, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatu, N., Hinning, L.G., Wynshaw-Boris, A., Yang, L., Yuan, Z., Zavolam, M., Shu, Y., Sarco, K., Shiraki, T., Konno, H., Nakamura, M., Sato, K., Shiraki, T., Waki, K., Sasaki, D., Sato, K., Shiraki, A., Yashingawa, J., Myazaki, A., Yashingawa, J., Myashin, Salaki, K., Sasaki, D., Shingawa, J., Maranabhi, A., Yashingawa, J., Waterston, R., Lander, B., Shiraki, M., Sasaki, D., Saibata, K., Shiraki, M., Sasaki, D., Saibata, K., Shiraki, M., Sasaki, D., Saibata, K., Shiraki, M., Sasaki, D., Saibata, K., Shiraki, M., Yashingawa, J., Myashingawa, J., Washingawa, J., Washing	Rogers, J., birmey, s. and mayashizaki, s. Analysis of the muranscriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002) 12466851
	RESULT 1 BY43389 LOCUS DETINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	AUTHORS	TITLE JOURNAL PUBMED

EST 02-JUL-2003

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Drosophila melanogaster genome survey sequence TET3 end of BAC:
BACR2DIO of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
AL067834
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/clone_lib="T.reese: mycelial culture, Version 3 april"
/note="vector: pREP3Y; Site_1: Not I/Sal I; Mycelial
culture grown from 24 hrs to 6 days with varying Carbon
and Nitrogen sources and concentrations."
                                                                                                                       B898978 sricol6xml0 T.reesei mycelial culture, Version 3 april Hypocrea ecorina cDNA clone tricol6xml0, mRNA sequence.
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1 (bases 1 to 80.7)

Foreman, P. K., Brown, D. E., Dankmeyer, L., Dean, R., Diener, S., Dun-Coleman, N. S., Goedegebuur, F., Houfek, T. D., England, G. J., Kelley, A. S., Meerman, H. J., Mitchill, T., Mitchinson, C., Olivares, H. A., Teunissen, P. J., Yao, J. and Mard, M.

Transcriptional regulation of biomass-degrading enzymes in the filamentous fungus Trichoderma reesei
J. Biol. Chem. 278 (34), 31988-31997 (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genencor Intl.
925 Page Mill Road, Palo Alto, CA 94304, USA
Tel: (650) 846-7635
Fax: (650) 621-7817
Email: Pforeman@genencor.com
Seq primer: LT-F1 primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Hypocrea jecorina"
/mol_type="mRNA"
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/clone="tric016xm10"
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                         Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1650 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

CNNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokchama Institute
Sciences Center (GSC), Yokchama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Tsurumi-ku, Yokchama, Kanagawa 230-0045, Japan Tel: 81-45-503-922
Fax: 81-45-503-9216
Email: genome-reseages riken.jp, URL:http://genome.gsc.riken.jp/
Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Pukuda, S.,
Hirozane, T., Imotani, K., Ishil, Y., Itoh, M., Kawai, J., Konno, H.,
Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,
Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,
Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and
Hayashizaki, Y. Direct Submission
Computational Analysis of Pull-Length Mouse CDNAS Compared with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="K630070123"
/clone=lib="RKKEN full-length enriched, pooled tissues, adult spleen, etc."
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Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neonate,tissue_type=thymus,sex=mix)
neonate,tissue_type=heart,sex=mix)'
Contact: Yoshihide Hayashizaki
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Matches 74; Conserv
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ORGANISM

VERSION KEYWORDS SOURCE

REFERENCE AUTHORS

JOURNAL

COMMENT

TITLE

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Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Bmail: sequenceGenoscope.cna.fr, Web : www.genoscope.cna.fr
18t strand CDNA was primed with a NotI-chigo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CV072680 406 bp mRNA linear EST 25-AUG-2004 Lr_JV2CF_27G04 SKplus Juvenile Earthworm Library Lumbricus rubellus CDNA clone Lr_JV2CF_27G04, mRNA sequence.
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Lumbricina; Lumbricidae; Lumbricus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue type="PLACENTA COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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Sequencing was performed in Edinburgh using the pBluescript II XR
cDNA library (Stratagene) protocol.
                                                                                                                                                                                                                                                                                                                                                                                                  For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSOAU013ZD11_U01236_1&c=7464.f. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chaseley,J., Hedley,B.A., Morgan,A.J., Sturzenbaum,S., Kille,P. Blaxter,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      195 CTCCTAGCCAAAATGCCCAGCGGTACTTCAAGAAGTACCAGAAACTCAAGGAGGCGGTCA
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Tel: +44 2920876680
Fax: +44 2920874305
Langth Country (C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization (Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14.1%; Scor.
54.3%; Pred. No. 4...
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI073YC17"
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Contact: Jennifer Chaseley
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                                                                                                                  Contact: Genoscope
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                                                                                                                                                                                                                                                                                                                                                                 - Web: www.genoscope.cns.fr.

- Web: www.genoscope.cns.fr.

- Web: www.genoscope.cns.fr.

- Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial BCORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and BST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be found at http://pacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BX368104 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CSODIO73YC17 3-PRIME, mkNA sequence.

BX368104 GI:30457686
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1051 TATTTTTTTTTTTTTTTTDHWMHWYTYTYTYTYTTCCCAHCYWMAAAWTTACCCCCCC 992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118 AAATGACCAGTCGAGTGTGCGGTTAGACAACTACTATACGGGCAAGGAACTGGAGATTGA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  178 GITGGATGTGGCTTTTGACTCCTAGCCAAAATGCCCAGCGGTACTTCAAGAAGTACCAGAA 237
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                            Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47; Mismatches
                                                                                          Drosophila melanogaster (fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="taxon:727"
/clone lib="RPCI-98"
/note="end : TET3"
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                                 AL067834.1 GI:4957863
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                                                                                                                                                                                                                                     (bases 1 to 1101)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 33.2%
Matches 68; Conservative
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                                                                                                                                                                                                                                                                                              Direct Submission
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Query Match

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/db xref="taxon:7165"
/dlone="19600449621565"
/dlone="19600449621565"
/dev stage="Addult"
/lab host="DH10b"
/clone_lib="A.Gam.ad.cDNA1"
/clone_lib="A.Gam.ad.cDNA1"
/note="vector: pSportl; Site_1: Sall; Site_2: Notl; Whole adult mosguitoes (mixed sax) frozen on liquid nitrogen.
cDNA inserts >500 bp cloned directionally into pSport 1.
Not 1 site is 3 . Clones available through the Malaria Research and Reference Reagent Resource Center (www.malaria.mr4.org)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST 26-FEB-2002
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/tissue_type="whole worm"
/dev_grage="adult"
/dev_grage="adult"
/clone_lib="Earthworm Lambda Zap Express Library"
/note="Vector: pBK-CMV; The library was prepared using protocol given by supplier (Stratagene)."
                                                                                                                                                                                                                                                                 160 CAAGGAACTGGAGATTGGATGTGGCTTTGACTCCTAGCCAAAATGCCCAGCGGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               160 CAAGGAACTGGAGATTGAGTTGGATGTGGCTTTGACTCCTAGCCAAAATGCCCAGCGGTA
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1 (bases 1 to 427)
Holt, R.A., Lin, J.-J., Murphy, S.D., Evans, C.A., Kraft, C.L., Charlab, R., Collins, F.H., Venter, J.C. and Hoffman, S.L. Celera Anopheles gambiae EST project
Unpublished (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BW638966 427 bp mRNA linear EST 26-
17000687567125 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone
19600449621565 5', mRNA sequence.
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                                                                                                                                                                                 Length 648;
                                                                                                                                                                            Score 36.8; DB 5; Length 64
Pred. No. 2.4;
0; Mismatches 27; Indels
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Anopheles gambiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Celera Genomics
45 w. Gude Dr., Rockville, MD 20850, USA
Tel: 2404533151
Fax: 2404534580
Email: HoltAM@celera.com
Email: HoltAM@celera.com
Elate: NU01004NBJ row: E column: 19
Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Anopheles gambiae"
/mol type="mRNA"
/strain="RSF-ST (Reduced susc.
chromosome)
                                                                                                                                                                                                                                                                                                                                                           220 CTTCAAGAAGTACCAGAAAC 239
                                                                                                                                                                                                                                                                                                                                                                                                     335 carcaagaagrrccagcaac 354
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                                                                                                                                                                              14.0%;
                                                                                                                                                                              Query Match
Best Local Similarity 66.2
Matches 53; Conservative
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BM638966
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97 CAACGAACTGGAGGTTGCCTTGGATGGAGCGAACAGGAGGACGCGCAGAGGAAGAA 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CA036082 Lt. adE 01G12_T3 Earthworm Lambda Zap Express Library Lumbricus rubellus CDNA clone Lr adE 01G12_5 similar to pir A59287 myosin heavy chain - fluke (Schistosoma mansoni) (strain Brazilian, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Blaxter ML
Institute of Call, Animal and Population Biology
University of Edinburgh
Ashworth Labs, King's Buildings, West Mains Road, Edinburgh, EH9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        160 CAAGGAACTGGAGATTGAGTTGGATGTGGCTTTGACTCCTAGCCAAAATGCCCAGCGGTA
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1 (bases 1 to 648)
Sturzenbaum, S., Parkinson, J., Blaxter, M., Morgan, J., Kille, P., Schaffner, W. and Georgiev, O.
Expressed Sequence Tags from the humus earthworm L. rubellus Unpublished (2000)
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Fax: +44 131 670 5450
Email: mark.blaxter@ed.ac.uk
The library was prepared using protocol given by supplier
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                                                                                                                                                                                                                                                                                                                                                                                                                                              14.0%; Score 36.8; DB 7; Length 406; 66.2%; Pred. No. 2.1; ive 0; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                    /dev_stage="Juvenile"
/clone_lib="Juvenile_Earthworm_Library"
/note="Organ: Whole_worm"
PCR PRimers
FORMARD: M13F (gttttcccagtcacgacg)
BACKWARD: M13F (caggaacagctatgaccatg)
Plate: 27 row: G column: 04
Seq primer: Skplus
High quality sequence start: 8
High quality sequence stop: 351.
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/organam="Lumbricus rubellus"
/mol_type="mRNA"
/db_xref="taxon:35632"
                                                                                                                                                                              1. .406
/organism="Lumbricus rubellus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lumbricus rubellus (humus earthworm)
Lumbricus rubellus
                                                                                                                                                                                                                                                                                                             tissue_type="Whole worm"
                                                                                                                                                                                                                      /mol type="mRNA"
/db xref="taxon:35632"
/clone="lr_JV2CF_27G04"
/sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plate: 01 row: G column: 12
Seq primer: T3
High quality sequence stop: 457.
Location/Qualifiers
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CA036082.1 GI:24334779
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Best Local Similarity
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CA036082
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Tel: 2404533151
Fax: 2404534580
Email: HoltRA@celera.com
                                                                                                                                                                                                                                                                                                                                                                                              chromosome) "
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Anopheles gambiae
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BM616582
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17000687562979 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone
19500496442127 5', mRNA sequence.
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//note="Vector: pSport1; Site_1: Sall; Site_2: Not1; Whole adult mosquitcos (mixed sex) frozen on liquid nitrogen.cDNA inserts >500 bp cloned directionally into pSport 1. Not 1 site is 3'. Clones available through the Malaria Research and Reference Reagent Resource Center (www.malaria.mr4.org)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            249 CAACGAGCTGGAGATTGCTCTGGATCACGCCAACAGGCTAACGCTGAGGCCCAGAAGAA 308
                                                                                                                                                                                                                                                 Anopheles gambiae (African malaria mosquito)
Anopheles gambiae
Rikaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Reptera; Endopterygota; Diptera; Nematocera; Culicoidea;
Culicidae; Anophelinae; Anopheles.
1 (bases 1 to 476)
3 1 (bases 1 to 476)
5 Holt, R.A., Lin, J.-J., Murphy, S.D., Evans, C.A., Kraft, C.L., Charlab, R., Collins, F.H., Venter, J.C. and Hoffman, S.L.
Celera Anopheles gambiae EST project
Unpublished (2002)
Contact: Holt R.A.
Celera Genomics
45 w. Gude Dr., Rockville, MD 20850, USA
Tel: 240453151
Pax: 240453151
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17000687309375 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone
18600449651236 5', mRNA sequence.
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Pred. No. 3.4;
0; Mismatches 38; Indels
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                                           271 CATCAAGCGCTACCAGCAGCAGCTGAAGGACGTCCAG 307
                      CTTCAAGAAGTACCAGAAACTCAAGGAGGCGGTCAAG 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/strain="RSP-ST (Reduced susc.
chromosome)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Anopheles gambiae"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bmail: HoltRA@celera.com
Plate: NU010049W6 row: J column: 02
Seg primer: M13 Reverge.
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/clone="19600449651236"
/dev_stage="Adult"
/lab_host="DH10b"
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BM642048.1 GI:18941559
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Best Local Similarity 60.8%;
Matches 59; Conservative (
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/clone="19600449642127"
/clone="19600449642127"
/clone="1960044064127"
/lab_host="Dello"
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/clone lib="A.Gam.ad.cDNA1"
/clone lib="A.Gam.ad.cDNA1"
/note="Vector: pSport1; Site 1: Sal1; Site 2: Not1; Whole adult mosquitoes (mixed sex) frozen on liquid nitrogen.
cDNA inserts >500 bp cloned directionally into pSport 1.
Not 1 site is 3'. Clones available through the Malaria
Research and Reference Reagent Resource Center
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17000687148935 A.Gam.ad.cDNA.bloodl Anopheles gambiae cDNA clone
18600449713643 5', mRNA sequence.
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Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea,
Culicidae, Anophelines, Anopheles.
1 (bases 1 to 578)
Holt.R.A., Lin,J.-J., Murphy,S.D., Evans,C.A., Kraft,C.L.,
Charlab,R., Collins,F.H., Venter,J.C. and Hoffman,S.L.
Celera Anopheles gambiae EST project
Unpublished (2002)
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae; Anophelinae; Anopheles.

1 (bases 1 to 486)
Holt, R.A., Lin, J.-J., Murphy, S.D., Evans, C.A., Kraft, C.L., Charlab, R., Collins, F.H., Venter, J.C. and Hoffman, S.L. Celera Anopheles gambiae EST project
Unpublished (2002)
Contact: Holt R.A.
Celera Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .486
/organism="Anopheles gambiae"
/mol_type="mRNA"
/strain="RSP-ST (Reduced susc. to Permethrin - std.
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Tel: 2404533151
Fax: 2404534580
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60.8%; Pred. No. 5...
0; Mismatches
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Plate: NUO1003CY2 row: N cc
Seg primer: M13 Reverse.
Location/Qualifiers
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/clone lib="A.Gam.ad.cDNA1"
/c
cDNA inserts >500 bp cloned directionally into pSport 1. Not 1 site is 3'. Clones available through the Malaria Research and Reference Reagent Resource Center (www.malaria.mr4.org)."
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1 (base 1 to 607)
Holt, R.A., Lin, J.-J., Murphy, S.D., Evans, C.A., Kraft, C.L., Charlab, R., Collins, F.H., Venter, J.C. and Hoffman, S.L. Colera Anopheles gambiae BST project
Contact: Holt R.A.
Celera Genomics

    .607
    /organism="Anopheles gambiae"
    /mol_type="mRNA"
    fstrain="RSP-ST (Reduced susc. to Permethrin - std. chromosome)"

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17000687497740 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone
19600449652861 5', mRNA sequence.
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0; Mismatches 38; Indels
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Tel: 2404533151
Fax: 2404534580
                                                                                                                                                                                            Query Match
13.8%; Score 36.2; DE
Best Local Similarity 60.8%; Pred. No. 3.6;
Matches 59; Conservative 0; Mismatches
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ilarity 60.8%; Pred. No. 3.4
Conservative 0; Mismatcher
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Plate: NU010049VE row: M
Seg primer: M13 Reverse.
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Best Local Similarity
Matches 59; Conserv
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JOURNAL
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="A.Gam.ad.cDNA.blood1"
/note="Vectors psport; Site_1: Sall, Site_2: Not1; Whole adult mosquitoes [mixed sex] frozen on liquid nitrogen 24 hours after human blood feeding. cDNA inserts >500 bp. cloned directionally into psport 1. Not 1 site is 3'. Clones available through the Malaria Research and Reference Reagent Resource Center (www.malaria.mr4.org)"
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Anopheles gambiae
Bukaryota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Culicoidea;
Culicidae; Anophelinae; Anopheles.
1 (Bases I to S85)
Holt, R.A., Lin, J.-J., Murphy, S.D., Evans, C.A., Kraft, C.L.,
Charlab, R., Collins, F.H., Venter, J.C. and Hoffman, S.L.
Celera Anopheles gambiae EST project
Contact: Holt R.A.
                                                                                                                                                                                                      to Permethrin - std.
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|mol_type="mRNA"
|strain="RSP-ST (Reduced susc. to Permethrin - std.
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17000687490727 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone
18600449669056 5', mRNA sequence.
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Fax: 2404534580
Email: HOLIERA@celera.com
Plate: NU01004AYV row: P column: 14
Seq primer: M13 Reverse.
                                                                                                                                                           /mol_type="mRNA"
/strain="RSP-ST (Reduced susc.
chromosome)"
                                                                                                                                   /organism≃"Anopheles gambiae"
          Plate: NU01004AXG row: A column: 21
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/clone="19600449713643"
                          Seq primer: M13 Reverse.
Location/Qualifiers
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Plate: NU01004185 row: K
Seq primer: M13 Reverse.
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cDNA inserts >500 bp cloned directionally into pSport 1.
Not i site is 3. clones available through the Malaria Research and Reference Reagent Resource Center (www.malaria.mr4.org)."
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                                                                                                            sm625696 610 bp mRNA linear EST 26-FEB-2002 17000687493467 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone 6500449628977 5', mRNA sequence.
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Anopheles gambiae
Rukaryota, Metazoa, Arthropoda, Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
Culicidae; Anophelinae; Anopheles.
I (bases 1 to 610)
Holt, R. A., Lin, J. -J., Murphy, S. D., Evans, C. A., Kraft, C. L.,
Charlab, R., Collins, F. H., Venter, J. C. and Hoffman, S. L.
Celera Anopheles gambiae EST project
Unpublished (2002)
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Anopheles gambiae
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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Fax: 2404534580
Faxi: 2404534580
Flami: HOUTRA@Celera.com
Plate: NU01004ABZ row: J column: 15
Seg primer: M13 Reverse.
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17000687439284 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone
19600449662409 5', mRNA sequence.
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Anopheles gambiae
Anopheles gambiae
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
Culicidae; Anophelinae; Anopheles.
1 (bases I to 630)
Holt,R.A., Lin,J.-J., Murphy,S.D., Evans,C.A., Kraft,C.L.,
Charlab,R., Collins,F.H., Venter,J.C. and Hoffman,S.L.
Celera Anopheles gambiae EST project
Unpublished (2002)
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Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culcidae; Anophelinae; Anopheles.

1 (bases 1 to 615)

1 (bases 1 to 615)

1 (bases 1 to 615)

1 (bases 1 to 615)

2 (barlab,R.A. Lin,J.-J. Murphy,S.D.; Evans,C.A.; Kraft,C.L., Charlab,R., Collins,P.H., Venter,J.C. and Hoffman,S.L.

Colera Anopheles gambiae EST project
Unpublished (2002)

Contact: Holt R.A.

Celera Genomics

45 w. Gude Dr., Rockville, MD 20850, USA

Tel: 240453151

Fax: 2404534580

Email: HoltRA@celera.com

Plate: NUO1004AZZ row: D column: 13

Seq primer: M13 Reverse
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/strain="RSP-ST (Reduced susc. to Permethrin - std.
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13.8%; Score 36.2; DB 3; Length 615;
Best Local Similarity 60.8%; Pred. No. 3.6;
Matches 59; Conservative 0; Mismatches 38; Indels
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Tel: 2404533151
Fax: 2404534580
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CDNA inserts >500 bp cloned directionally into pSport 1.
Not 1 site is 3'. Clones available through the Malaxia Research and Reference Reagent Resource Center (www.malaria.mr4.org)."
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Location/Qualifiers
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